has been amended to further specify that the claimed kit includes a reference that provides information regarding location/analyte identity. Support for this amendment is found in the specification at page 35, line 27 to page 36, line 2, and elsewhere. Finally, the array claim has been amended to specify that at least one of the tag complements is hybridized to a tagged affinity ligand, where the tagged affinity ligand includes an antibody or fragment thereof, where support for this amendment is found in copending Claim 12, among other locations in the specification. The attached marked up version is captioned, **"Version With Markings To Show Changes Made."** As the above amendments find support in the specification, they introduce no new matter and their entry by the Examiner is respectfully requested.

Claims 1, 4-10, 12, 13, 15, 16 and 18-21 were first rejected under 35 U.S.C. § 112, 2nd ¶ for a number of issues. It is believed that the above amendments address each of the issues raised by the Examiner. Accordingly, it is respectfully submitted that this rejection may be withdrawn.

Claim 1 has been rejected under 35 U.S.C. § 102(b) as being anticipated by Brenner. As amended, Claim 1 requires that one identify the presence of an analyte in a sample by using information regarding both the presence and location of a tagged affinity ligand/analyte complex on the surface of an array. Nowhere in Brenner is there taught (or even suggested) a step of relating information about the location of a complex on a substrate surface to the identity of the analyte in the complex at that location. Such a teaching is absent because Brenner is merely a method of sorting nucleic acids, where the substrate can be a bead or an array, and location on the substrate is not even employed in Brenner's methods. As such, Brenner fails to anticipate the claimed invention and this rejection may be withdrawn.

Claim 1 has been rejected under 35 U.S.C. § 102(e) as being anticipated by Kamb.

As amended, Claim 1 requires that one identify the presence of an analyte in a sample by using information regarding both the presence and location of a tagged affinity ligand/analyte complex on the surface of an array. Nowhere in Kamb is there taught (or even suggested) a step of relating information about the location of a complex on a substrate surface to the identity of the analyte in the complex at that location. Such a teaching is absent because Kamb is merely a method of sorting nucleic acids and

comparing amounts thereof, where the substrate is a bead and location on the substrate is not even employed in Kamb's methods. As such, Kamb fails to anticipate the claimed invention and this rejection may be withdrawn.

Claims 4-9 have been rejected under 35 U.S.C. § 103(a) over Brenner or Kamb in view of Shannon and Lockhart. As explained above, both Brenner and Kamb fail to teach the basic method as claimed in that they fail to teach, or even suggest, a method where location of a complex on a surface is employed to determine the identity of the analyte in the sample. The supplemental references have been cited solely for the hybridization efficiency limitation, these references fail to make up the fundamental deficiency in both Brenner and Kamb. As such, Claims 4-9 are not obvious under 35 U.S.C. § 103(a) over Brenner or Kamb in view of Shannon and Lockhart and this rejection may be withdrawn.

Claims 10, 12, 13 and 15 have been rejected under 35 U.S.C. § 103(a) over Kamb in view of Burmer. As explained above, Kamb fails to teach the basic method as claimed in that Kamb fails to teach, or even suggest, a method where location of a complex on a surface is employed to determine the identity of the analyte in the sample. The supplemental Burmer reference has been cited solely for the teaching of a peptide analyte, and therefore fails to make up the fundamental deficiency in Kamb. As such, Claims 10, 12, 13 and 15 are not obvious under 35 U.S.C. § 103(a) over Kamb in view of Burmer and this rejection may be withdrawn.

Claims 16, 18-22 and 24 have been rejected under 35 U.S.C. § 103(a) over Kamb in view of Shannon and Lockhart, Burmer and Brown et al. As explained above, Kamb fails to teach the basic method as claimed in that Kamb fails to teach, or even suggest, a method where location of a complex on a surface is employed to determine the identity of the analyte in the sample. The supplemental references have been cited solely for elements appearing in various dependent claims, and these references fail to make up the fundamental deficiency in Kamb. As such, Claims 16. 18-22 and 24 are not obvious under 35 U.S.C. § 103(a) over Kamb in view of Shannon and Lockhart, Burmer and Brown and this rejection may be withdrawn.

Finally, Claims 1, 4-9, 13, 15, 16, 18-22 and 24 have been provisionally rejected under the judicially created doctrine of obviousness type double patenting as being

unpatentable over Claims 1-5, 7-13, 15-19 and 22 of copending application serial no. 09/752,293. Solely in order to expedite allowance of the present application, enclosed please find a Terminal Disclaimer, in view of which this rejection may be withdrawn.

In view of the above amendments and remarks, this application is considered to be in good and proper form for allowance and the Examiner is respectfully requested to pass this application to issue.

If, in the opinion of the Examiner, a telephonic interview would expedite prosecution of this application, the Examiner is invited to contact the undersigned at (650) 833-7770.

If the Patent Office determines that fees, including extensions of time, are required, the Applicants hereby petition for any required relief, including extensions of time, and authorize the Commissioner to charge the cost of such to our Deposit Account No. 50-0815, Order No. CLON-017US2.

Respectfully Submitted,

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enc:

- Terminal Disclaimer over U.S. Application Serial No. 09/752,293

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Version With Markings To Show Changes Made

IN THE CLAIMS

1. (Twice Amended) A method of ~~detecting~~ identifying the presence of at least one analyte in a sample, said method comprising:

(a) contacting said sample with a population of tagged affinity ligands under conditions sufficient to produce ~~said as~~ at least one analyte/tagged affinity ligand complex;

(b) contacting said at least one analyte/tagged affinity ligand complex produced in step (a) with an array of tag complements under hybridization conditions to produce at least one surface bound hybridization complex;

(c) detecting the presence and location of said at least one surface bound hybridization complex; and

(d) identifying ~~thereby detecting~~ the presence of said at least one analyte in said sample from said detected presence and location of said at least one surface bound hybridization complex.

7. (Once Amended) The method according to Claim 1 ~~3~~, wherein any tag employed in said assay has a level of cross-hybridization that does not exceed about 10%.

15. (Once Amended) The method according to Claim 1 ~~14~~, wherein said plurality of analytes are proteins.

16. (Twice Amended) A kit for use in an analyte detection assay, said kit comprising:

(a) an array of distinct tag complements immobilized on the surface of a ~~sold~~ solid support;

(b) a set of distinct tagged affinity ligands, wherein each member of said set comprises a tag that hybridizes to a tag complement of said array; ~~and~~

(c) means for identifying the physical location on said array to which each distinct tagged affinity ligand of said set hybridizes; and

(d) a reference that provides information correlating each location on said array to a particular analyte.

22. (Twice Amended) An array of distinct tag complements immobilized on a solid support, wherein said tag complements are members of a collection of tag-tag

complement pairs in which the magnitude of any difference in hybridization efficiency between any two tag-tag complements pairs in said collection does not exceed about 10 fold and at least one of said tag complements of said array is hybridized to a tagged affinity ligand comprising an antibody or binding fragment thereof.